

RAW SEQUENCE LISTING

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Application Serial Number: 10/691,672A

Source: IFWJ0

Date Processed by STIC: 1/28/05

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IFWO

RAW SEQUENCE LISTING

DATE: 01/28/2005

PATENT APPLICATION: US/10/691,672A

TIME: 16:07:53

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Output Set: N:\CRF4\01282005\J691672A.raw

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3 <110> APPLICANT: DRUILHE, PIERRE
5 <120> TITLE OF INVENTION: GLURP-MSP3 FUSION PROTEIN, IMMUNOGENIC COMPOSITIONS AND
6   MALARIAL VACCINES CONTAINING IT
8 <130> FILE REFERENCE: 02356.0085
10 <140> CURRENT APPLICATION NUMBER: 10/691,672A
11 <141> CURRENT FILING DATE: 2003-10-24
13 <160> NUMBER OF SEQ ID NOS: 13
15 <170> SOFTWARE: PatentIn Ver. 3.3
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 491
19 <212> TYPE: PRT
20 <213> ORGANISM: Plasmodium falciparum
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23 <221> NAME/KEY: SITE
24 <222> LOCATION: (1)..(491)
25 <223> OTHER INFORMATION: GLURP amino acids 24-514
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32           20           25           30
34 Gly Lys Ile Ile Arg Gly Ser Asn Asp Lys Leu Asn Lys Asn Ser Glu
35           35           40           45
37 Asp Val Leu Glu Gln Ser Glu Lys Ser Leu Val Ser Glu Asn Val Pro
38           50           55           60
40 Ser Gly Leu Asp Ile Asp Asp Ile Pro Lys Glu Ser Ile Phe Ile Gln
41   65           70           75           80
43 Glu Asp Gln Glu Gly Gln Thr His Ser Glu Leu Asn Pro Glu Thr Ser
44           85           90           95
46 Glu His Ser Lys Asp Leu Asn Asn Asn Asp Ser Lys Asn Glu Ser Ser
47           100          105          110
49 Asp Ile Ile Ser Val Asn Asn Lys Ser Asn Lys Val Gln Asn His Phe
50           115          120          125
52 Glu Ser Leu Ser Asp Leu Glu Leu Leu Glu Asn Ser Ser Gln Asp Asn
53           130          135          140
55 Leu Asp Lys Asp Thr Ile Ser Thr Glu Pro Phe Pro Asn Gln Lys His
56   145          150          155          160
58 Lys Asp Leu Gln Gln Asp Leu Asn Asp Glu Pro Leu Glu Pro Phe Pro
59           165          170          175
61 Thr Gln Ile His Lys Asp Tyr Lys Glu Lys Asn Leu Ile Asn Glu Glu
62           180          185          190
64 Asp Ser Glu Pro Phe Pro Arg Gln Lys His Lys Lys Val Asp Asn His
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68      210                      215                      220
70 Gln Gly Ser Leu Lys Leu Lys Ser Phe Asp Glu His Leu Lys Asp Glu
71 225                      230                      235                      240
73 Lys Ile Glu Asn Glu Pro Leu Val His Glu Asn Leu Ser Ile Pro Asn
74      245                      250                      255
76 Asp Pro Ile Glu Gln Ile Leu Asn Gln Pro Glu Gln Glu Thr Asn Ile
77      260                      265                      270
79 Gln Glu Gln Leu Tyr Asn Glu Lys Gln Asn Val Glu Glu Lys Gln Asn
80      275                      280                      285
82 Ser Gln Ile Pro Ser Leu Asp Leu Lys Glu Pro Thr Asn Glu Asp Ile
83      290                      295                      300
85 Leu Pro Asn His Asn Pro Leu Glu Asn Ile Lys Gln Ser Glu Ser Glu
86 305                      310                      315                      320
88 Ile Asn His Val Gln Asp His Ala Leu Pro Lys Glu Asn Ile Ile Asp
89      325                      330                      335
91 Lys Leu Asp Asn Gln Lys Glu His Ile Asp Gln Ser Gln His Asn Ile
92      340                      345                      350
94 Asn Val Leu Gln Glu Asn Asn Ile Asn Asn His Gln Leu Glu Pro Gln
95      355                      360                      365
97 Glu Lys Pro Asn Ile Glu Ser Phe Glu Pro Lys Asn Ile Asp Ser Glu
98      370                      375                      380
100 Ile Ile Leu Pro Glu Asn Val Glu Thr Glu Glu Ile Ile Asp Asp Val
101 385                      390                      395                      400
103 Pro Ser Pro Lys His Ser Asn His Glu Thr Phe Glu Glu Glu Thr Ser
104      405                      410                      415
106 Glu Ser Glu His Glu Glu Ala Val Ser Glu Lys Asn Ala His Glu Thr
107      420                      425                      430
109 Val Glu His Glu Glu Thr Val Ser Gln Glu Ser Asn Pro Glu Lys Ala
110      435                      440                      445
112 Asp Asn Asp Gly Asn Val Ser Gln Asn Ser Asn Asn Glu Leu Asn Glu
113      450                      455                      460
115 Asn Glu Phe Val Glu Ser Glu Lys Ser Glu His Glu Pro Ala Glu Asn
116 465                      470                      475                      480
118 Glu Glu Ser Ser Leu Glu Glu Gly His His Glu
119      485                      490
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124 <212> TYPE: PRT
125 <213> ORGANISM: Plasmodium falciparum
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129 <222> LOCATION: (1)..(169)
130 <223> OTHER INFORMATION: MSP3 amino acids 212-380
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134 1                      5                      10                      15
136 Gly Val Pro Glu His Lys Lys Glu Glu Asn Met Leu Ser His Leu Tyr
137      20                      25                      30

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139 Val Ser Ser Lys Asp Lys Glu Asn Ile Ser Lys Glu Asn Asp Asp Val
140          35          40          45
142 Leu Asp Glu Lys Glu Glu Glu Ala Glu Glu Thr Glu Glu Glu Glu Leu
143          50          55          60
145 Glu Glu Lys Asn Glu Glu Glu Thr Glu Ser Glu Ile Ser Glu Asp Glu
146 65          70          75          80
148 Glu Glu Glu Glu Glu Glu Glu Lys Glu Glu Glu Asn Glu Lys Lys Lys
149          85          90          95
151 Glu Gln Glu Lys Glu Gln Ser Asn Glu Asn Asn Asp Gln Lys Lys Asp
152          100          105          110
154 Met Glu Ala Gln Asn Leu Ile Ser Lys Asn Gln Asn Asn Asn Glu Lys
155          115          120          125
157 Asn Val Lys Glu Ala Ala Glu Ser Ile Met Lys Thr Leu Ala Gly Leu
158          130          135          140
160 Ile Lys Gly Asn Asn Gln Ile Asp Ser Thr Leu Lys Asp Leu Val Glu
161 145          150          155          160
163 Glu Leu Ser Lys Tyr Phe Lys Asn His
164          165
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176 <220> FEATURE:
177 <221> NAME/KEY: SITE
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179 <223> OTHER INFORMATION: GLURP MSP3 fusion protein
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186          20          25          30
188 Ile Arg Gly Ser Asn Asp Lys Leu Asn Lys Asn Ser Glu Asp Val Leu
189          35          40          45
191 Glu Gln Ser Glu Lys Ser Leu Val Ser Glu Asn Val Pro Ser Gly Leu
192          50          55          60
194 Asp Ile Asp Asp Ile Pro Lys Glu Ser Ile Phe Ile Gln Glu Asp Gln
195 65          70          75          80
197 Glu Gly Gln Thr His Ser Glu Leu Asn Pro Glu Thr Ser Glu His Ser
198          85          90          95
200 Lys Asp Leu Asn Asn Asn Gly Ser Lys Asn Glu Ser Ser Asp Ile Ile
201          100          105          110
203 Ser Glu Asn Asn Lys Ser Asn Lys Val Gln Asn His Phe Glu Ser Leu
204          115          120          125
206 Ser Asp Leu Glu Leu Leu Glu Asn Ser Ser Gln Asp Asn Leu Asp Lys
207          130          135          140
209 Asp Thr Ile Ser Thr Glu Pro Phe Pro Asn Gln Lys His Lys Asp Leu

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213					165					170					175	
215	His	Lys	Asp	Tyr	Lys	Glu	Lys	Asn	Leu	Ile	Asn	Glu	Glu	Asp	Ser	Glu
216				180					185					190		
218	Pro	Phe	Pro	Arg	Gln	Lys	His	Lys	Lys	Val	Asp	Asn	His	Asn	Glu	Glu
219			195					200				205				
221	Lys	Asn	Val	Phe	His	Glu	Asn	Gly	Ser	Ala	Asn	Gly	Asn	Gln	Gly	Ser
222		210					215					220				
224	Leu	Lys	Leu	Lys	Ser	Phe	Asp	Glu	His	Leu	Lys	Asp	Glu	Lys	Ile	Glu
225	225					230					235					240
227	Asn	Glu	Pro	Leu	Val	His	Glu	Asn	Leu	Ser	Ile	Pro	Asn	Asp	Pro	Ile
228				245					250					255		
230	Glu	Gln	Ile	Leu	Asn	Gln	Pro	Glu	Gln	Glu	Thr	Asn	Ile	Gln	Glu	Gln
231			260						265					270		
233	Leu	Tyr	Asn	Glu	Lys	Gln	Asn	Val	Glu	Glu	Lys	Gln	Asn	Ser	Gln	Ile
234		275					280					285				
236	Pro	Ser	Leu	Asp	Leu	Lys	Glu	Pro	Thr	Asn	Glu	Asp	Ile	Leu	Pro	Asn
237		290					295					300				
239	His	Asn	Pro	Leu	Glu	Asn	Ile	Lys	Gln	Ser	Glu	Ser	Glu	Ile	Asn	His
240	305				310					315						320
242	Val	Gln	Asp	His	Ala	Leu	Pro	Lys	Glu	Asn	Ile	Ile	Asp	Lys	Leu	Asp
243				325					330					335		
245	Asn	Gln	Lys	Glu	His	Ile	Asp	Gln	Ser	Gln	His	Asn	Ile	Asn	Val	Leu
246			340						345				350			
248	Gln	Glu	Asn	Asn	Ile	Asn	Asn	His	Gln	Leu	Glu	Pro	Gln	Glu	Lys	Pro
249			355					360					365			
251	Asn	Ile	Glu	Ser	Phe	Glu	Pro	Lys	Asn	Ile	Asp	Ser	Glu	Ile	Ile	Leu
252		370					375					380				
254	Pro	Glu	Asn	Val	Glu	Thr	Glu	Glu	Ile	Ile	Asp	Asp	Val	Pro	Ser	Pro
255	385					390					395					400
257	Lys	His	Ser	Asn	His	Glu	Thr	Phe	Glu	Glu	Glu	Thr	Ser	Glu	Ser	Glu
258				405					410					415		
260	His	Glu	Glu	Ala	Val	Ser	Glu	Lys	Asn	Ala	His	Glu	Thr	Val	Glu	His
261			420						425					430		
263	Glu	Glu	Thr	Val	Ser	Gln	Glu	Ser	Asn	Pro	Glu	Lys	Ala	Asp	Asn	Asp
264			435					440					445			
266	Gly	Asn	Val	Ser	Gln	Asn	Ser	Asn	Asn	Glu	Leu	Asn	Glu	Asn	Glu	Phe
267		450				455						460				
269	Val	Glu	Ser	Glu	Lys	Ser	Glu	His	Glu	Ala	Arg	Ser	Lys	Ala	Lys	Glu
270	465					470					475					480
272	Ala	Ser	Ser	Tyr	Asp	Tyr	Ile	Leu	Gly	Trp	Glu	Phe	Gly	Gly	Gly	Val
273				485					490					495		
275	Pro	Glu	His	Lys	Lys	Glu	Glu	Asn	Met	Leu	Ser	His	Leu	Tyr	Val	Ser
276				500					505					510		
278	Ser	Lys	Asp	Lys	Glu	Asn	Ile	Ser	Lys	Glu	Asn	Asp	Asp	Val	Leu	Asp
279			515					520					525			
281	Glu	Lys	Glu	Glu	Glu	Ala	Glu	Glu	Thr	Glu	Glu	Glu	Glu	Leu	Glu	Glu
282		530					535					540				

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284 Lys Asn Glu Glu Glu Thr Glu Ser Glu Ile Ser Glu Asp Glu Glu Glu
285 545                               550                               555                               560
287 Glu Glu Glu Glu Glu Lys Glu Glu Glu Asn Glu Lys Lys Lys Glu Gln
288                               565                               570                               575
290 Glu Lys Glu Gln Ser Asn Glu Asn Asn Asp Gln Lys Lys Asp Met Glu
291                               580                               585                               590
293 Ala Gln Asn Leu Ile Ser Lys Asn Gln Asn Asn Asn Glu Lys Asn Val
294                               595                               600                               605
296 Lys Glu Ala Ala Glu Ser Ile Met Lys Thr Leu Ala Gly Leu Ile Lys
297                               610                               615                               620
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300 625                               630                               635                               640
302 Ser Lys Tyr Phe Lys Asn His
303                               645
306 <210> SEQ ID NO: 4
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308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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315 <400> SEQUENCE: 4
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318 aataaaaaact ctgaagatgt tttagaacaa agcgaaaaat cgcttgtttc agaaaatgtt 180
319 cctagtggat tagatataga tgatatccct aaagaatcta tttttattca agaagatcaa 240
320 gaaggtcaaaa ctcatcttga attaaatcct gaaacatcag aacatagtaa agatttaaat 300
321 aataatgggtt caaaaaatga atctagtgat attatttcag aaaataataa atcaaatataa 360
322 gtacaaaatc attttgaatc attatcagat ttagaattac ttgaaaattc ctcacaagat 420
323 aatttagaca aagatacaat ttcaacagaa ccttttccta atcaaaaaca taaagactta 480
324 caacaagatt taaatgatga accttttagaa ccctttccta cacaaatata taaagattat 540
325 aaagaaaaaaa atttaataaaa tgaagaagat tcagaaccat ttcccagaca aaagcataaa 600
326 aaggtagaca atcataatga agaaaaaaac gtatttcattg aaaatgggttc tgcaaatggg 660
327 aatcaaggaa gtttgaaact taaatcattc gatgaacatt taaaagatga aaaaatagaa 720
328 aatgaaccac ttgttcattga aaatttatcc ataccaaatg atccaataga acaaatatta 780
329 aatcaacctg aacaagaaac aaatatccag gaacaattgt ataatgaaaa acaaatgtt 840
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331 atttttacca atcataatcc attagaaaat ataaaacaaa gtgaatcaga aataaatcat 960
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334 caattagaac ctcaagagaa acctaatatt gaatcgtttg aacctaaaaa tatagattca 1140
335 gaaattattc ttcttgaaaa tgttgaaaca gaagaaataa tagatgatgt gccttcccct 1200
336 aaacattcta accatgaaac atttgaagaa gaaacaagtg aatctgaaca tgaagaagcc 1260
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341 aaagaagaaa atatgttatc acatttatat gtttcttcaa aggataagga aatatatatc 1560
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VERIFICATION SUMMARY

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